



SEQUENCE LISTING

<110> FUJITA, JUN

<120> GANKYRIN

<130> 053466/0277

<140> 09/509,775

<141> 2000-03-31

<150> PCT/JP98/04467

<151> 1998-10-02

<150> JP 9-286214

<151> 1997-03-10

<160> 16

<170> PatentIn Ver. 2.1

<210> 1

<211> 780

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (97)..(774)

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Met Glu Gly Cys Val Ser
1 5aac cta atg gtc tgc aac ctg gcc tac agc ggg aag ctg gaa gag ttg 162
Asn Leu Met Val Cys Asn Leu Ala Tyr Ser Gly Lys Leu Glu Glu Leu
10 15 20aag gag agt att ctg gcc gat aaa tcc ctg gct act aga act gac cag 210
Lys Glu Ser Ile Leu Ala Asp Lys Ser Leu Ala Thr Arg Thr Asp Gln
25 30 35gac agc aga act gca ttg cac tgg gca tgc tca gct gga cat aca gaa 258
Asp Ser Arg Thr Ala Leu His Trp Ala Cys Ser Ala Gly His Thr Glu
40 45 50att gtt gaa ttt ttg caa ctt gga gtg cca gtg aat gat aaa gac 306
Ile Val Glu Phe Leu Leu Gln Leu Gly Val Pro Val Asn Asp Lys Asp
55 60 65 70gat gca ggt tgg tct cct ctt cat att gcg gct tct gct ggc cgg gat 354
Asp Ala Gly Trp Ser Pro Leu His Ile Ala Ala Ser Ala Gly Arg Asp
75 80 85

gag att gta aaa gcc ctt ctg gga aaa ggt gct caa gtg aat gct gtc		402	
Glu Ile Val Lys Ala Leu Leu Gly Lys Gly Ala Gln Val Asn Ala Val			
90	95	100	
aat caa aat ggc tgt act ccc tta cat tat gca gct tcg aaa aac agg		450	
Asn Gln Asn Gly Cys Thr Pro Leu His Tyr Ala Ala Ser Lys Asn Arg			
105	110	115	
cat gag atc gct gtc atg tta ctg gaa ggc ggg gct aat cca gat gct		498	
His Glu Ile Ala Val Met Leu Leu Glu Gly Ala Asn Pro Asp Ala			
120	125	130	
aag gac cat tat gag gct aca gca atg cac cgg gca gca gcc aag ggt		546	
Lys Asp His Tyr Glu Ala Thr Ala Met His Arg Ala Ala Lys Gly			
135	140	145	150
aac ttg aag atg att cat atc ctt ctg tac tac aaa gca tcc aca aac		594	
Asn Leu Lys Met Ile His Ile Leu Leu Tyr Tyr Lys Ala Ser Thr Asn			
155	160	165	
atc caa gac act gag ggt aac act cct cta cac tta gcc tgt gat gag		642	
Ile Gln Asp, Thr Glu Gly Asn Thr Pro Leu His Leu Ala Cys Asp Glu			
170	175	180	
gag aga gtg gaa gaa gca aaa ctg ctg gtg tcc caa gga gca agt att		690	
Glu Arg Val Glu Glu Ala Lys Leu Leu Val Ser Gln Gly Ala Ser Ile			
185	190	195	
tac att gag aat aaa gaa gaa aag aca ccc ctg caa gtg gcc aaa ggt		738	
Tyr Ile Glu Asn Lys Glu Glu Lys Thr Pro Leu Gln Val Ala Lys Gly			
200	205	210	
ggc ctg ggt tta ata ctc aag aga atg gtg gaa ggt taaaaca		780	
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215	220	225	

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<212> PRT
<213> Homo sapiens

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Gly Lys Leu Glu Glu Leu Lys Glu Ser Ile Leu Ala Asp Lys Ser Leu			
20	25	30	
Ala Thr Arg Thr Asp Gln Asp Ser Arg Thr Ala Leu His Trp Ala Cys			
35	40	45	
Ser Ala Gly His Thr Glu Ile Val Glu Phe Leu Leu Gln Leu Gly Val			
50	55	60	
Pro Val Asn Asp Lys Asp Asp Ala Gly Trp Ser Pro Leu His Ile Ala			
65	70	75	80

Ala Ser Ala Gly Arg Asp Glu Ile Val Lys Ala Leu Leu Gly Lys Gly
 85 90 95

Ala Gln Val Asn Ala Val Asn Gln Asn Gly Cys Thr Pro Leu His Tyr
 100 105 110

Ala Ala Ser Lys Asn Arg His Glu Ile Ala Val Met Leu Leu Glu Gly
 115 120 125

Gly Ala Asn Pro Asp Ala Lys Asp His Tyr Glu Ala Thr Ala Met His
 130 135 140

Arg Ala Ala Ala Lys Gly Asn Leu Lys Met Ile His Ile Leu Leu Tyr
 145 150 155 160

Tyr Lys Ala Ser Thr Asn Ile Gln Asp Thr Glu Gly Asn Thr Pro Leu
 165 170 175

His Leu Ala Cys Asp Glu Glu Arg Val Glu Glu Ala Lys Leu Leu Val
 180 185 190

Ser Gln Gly Ala Ser Ile Tyr Ile Glu Asn Lys Glu Glu Lys Thr Pro
 195 200 205

Leu Gln Val Ala Lys Gly Gly Leu Gly Leu Ile Leu Lys Arg Met Val
 210 215 220

Glu Gly
 225

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 <213> Mus sp.

<220>
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 <222> (1)...(693)

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 Met Glu Gly Cys Val Ser Asn Ile Met Ile Cys Asn Leu Ala Tyr Ser
 1 5 10 15

ggg aag ctg gat gag ttg aag gag cgcc att ttg gct gat aaa tct ctg 96
 Gly Lys Leu Asp Glu Leu Lys Glu Arg Ile Leu Ala Asp Lys Ser Leu
 20 25 30

gct act aga act gat cag gac aga aca gct ttg cac tgg gca tgc 144
 Ala Thr Arg Thr Asp Gln Asp Ser Arg Thr Ala Leu His Trp Ala Cys
 35 40 45

tca gct ggc cat aca gaa att gtt gaa ttc ttg ctg caa ctt gga gtg Ser Ala Gly His Thr Glu Ile Val Glu Phe Leu Leu Gln Leu Gly Val	192	
50 55 60		
cca gtn aat gat aaa gat gac gca ggt tgg tct cct ctt cat att gct Pro Val Asn Asp Lys Asp Asp Ala Gly Trp Ser Pro Leu His Ile Ala	240	
65 70 75 80		
gcc tcc gct ggc cg ^g gat gag att gta aaa gcc ctt ctg gtg aaa ggt Ala Ser Ala Gly Arg Asp Glu Ile Val Lys Ala Leu Leu Val Lys Gly	288	
85 90 95		
gca cat gtt aat tct gtc aat caa aac ggc tgc act cca ctc cat tat Ala His Val Asn Ser Val Asn Gln Asn Gly Cys Thr Pro Leu His Tyr	336	
100 105 110		
gca gct tcg aag aat agg cat gag att tct gtt atg tta cta gaa ggt Ala Ala Ser Lys Asn Arg His Glu Ile Ser Val Met Leu Leu Glu Gly	384	
115 120 125		
ggg gct aac cca gat gcg aag gac cat tac gat gct aca gca atg cac Gly Ala Asn Pro Asp Ala Lys Asp His Tyr Asp Ala Thr Ala Met His	432	
130 135 140		
cgg gca gca gcc aag ggt aac ttg aag atg gtt cac atc ctt ctg ttc Arg Ala Ala Ala Lys Gly Asn Leu Lys Met Val His Ile Leu Leu Phe	480	
145 150 155 160		
tac aaa gca tcc aca aac atc caa gac act gag ggt aac act cct cta Tyr Lys Ala Ser Thr Asn Ile Gln Asp Thr Glu Gly Asn Thr Pro Leu	528	
165 170 175		
cac tta gcc tgt gat gaa gag aga gtg gaa gag gca aaa ttt ctg gtg His Leu Ala Cys Asp Glu Glu Arg Val Glu Glu Ala Lys Phe Leu Val	576	
180 185 190		
act caa gga gca agt att tac att gag aat aaa gaa gaa aag aca ccc Thr Gln Gly Ala Ser Ile Tyr Ile Glu Asn Lys Glu Glu Lys Thr Pro	624	
195 200 205		
ctg caa gtt gcc aaa ggg ggc ctg ggt tta ata ctc aag aga cta gca Leu Gln Val Ala Lys Gly Gly Leu Gly Leu Ile Leu Lys Arg Leu Ala	672	
210 215 220		
gaa agt gaa gag gct tct atg tag Glu Ser Glu Glu Ala Ser Met	696	
225 230		
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Gly Lys Leu Asp Glu Leu Lys Glu Arg Ile Leu Ala Asp Lys Ser Leu
 20 25 30

Ala Thr Arg Thr Asp Gln Asp Ser Arg Thr Ala Leu His Trp Ala Cys
 35 40 45

Ser Ala Gly His Thr Glu Ile Val Glu Phe Leu Leu Gln Leu Gly Val
 50 55 60

Pro Val Asn Asp Lys Asp Asp Ala Gly Trp Ser Pro Leu His Ile Ala
 65 70 75 80

Ala Ser Ala Gly Arg Asp Glu Ile Val Lys Ala Leu Leu Val Lys Gly
 85 90 95

Ala His Val Asn Ser Val Asn Gln Asn Gly Cys Thr Pro Leu His Tyr
 100 105 110

Ala Ala Ser Lys Asn Arg His Glu Ile Ser Val Met Leu Leu Glu Gly
 115 120 125

Gly Ala Asn Pro Asp Ala Lys Asp His Tyr Asp Ala Thr Ala Met His
 130 135 140

Arg Ala Ala Ala Lys Gly Asn Leu Lys Met Val His Ile Leu Leu Phe
 145 150 155 160

Tyr Lys Ala Ser Thr Asn Ile Gln Asp Thr Glu Gly Asn Thr Pro Leu
 165 170 175

His Leu Ala Cys Asp Glu Glu Arg Val Glu Glu Ala Lys Phe Leu Val
 180 185 190

Thr Gln Gly Ala Ser Ile Tyr Ile Glu Asn Lys Glu Glu Lys Thr Pro
 195 200 205

Leu Gln Val Ala Lys Gly Leu Gly Leu Ile Leu Lys Arg Leu Ala
 210 215 220

Glu Ser Glu Glu Ala Ser Met
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20 25 30	
gcc act aga act gat cag gac agc aga aca gca ttg cac tgg gca tgc Ala Thr Arg Thr Asp Gln Asp Ser Arg Thr Ala Leu His Trp Ala Cys	144
35 40 45	
tca gct ggt cat aca gaa att gtt gaa ttc ttg ctg caa ctt gga gtg Ser Ala Gly His Thr Glu Ile Val Phe Leu Leu Gln Leu Gly Val	192
50 55 60	
cca gta aat gaa aaa gac gat gca ggt tgg tct cct ctt cat att gct Pro Val Asn Glu Lys Asp Asp Ala Gly Trp Ser Pro Leu His Ile Ala	240
65 70 75 80	
gct tcc gct ggc cg ^g gat gag att gta aaa gcc ctt ctg ata aaa ggg Ala Ser Ala Gly Arg Asp Glu Ile Val Lys Ala Leu Leu Ile Lys Gly	288
85 90 95	
gca caa gtg aat gcc gtc aat cag aat ggc tgc acg gcc ctt cat tat Ala Gln Val Asn Ala Val Asn Gln Asn Gly Cys Thr Ala Leu His Tyr	336
100 105 110	
gca gct tcc aag aat agg cat gag att gct gtt atg tta cta gaa ggt Ala Ala Ser Lys Asn Arg His Glu Ile Ala Val Met Leu Leu Glu Gly	384
115 120 125	
ggg gct aat cca gat gct aag aac cat tat gat gct aca gca atg cac Gly Ala Asn Pro Asp Ala Lys Asn His Tyr Asp Ala Thr Ala Met His	432
130 135 140	
cgg gca gca gcc aag ggt aac ttg aag atg gtt cat atc ctt ctg ttc Arg Ala Ala Ala Lys Gly Asn Leu Lys Met Val His Ile Leu Leu Phe	480
145 150 155 160	
tac aaa gca tcc aca aac atc caa gat act gag ggt aac act cct cta Tyr Lys Ala Ser Thr Asn Ile Gln Asp Thr Glu Gly Asn Thr Pro Leu	528
165 170 175	
cac tta gcc tgt gat gag gag aga gtg gaa gaa gca aaa ttg ctg gtg His Leu Ala Cys Asp Glu Glu Arg Val Glu Glu Ala Lys Leu Leu Val	576
180 185 190	
acc caa gga gca agt att tac att gaa aat aag gaa gaa aag aca ccg Thr Gln Gly Ala Ser Ile Tyr Ile Glu Asn Lys Glu Glu Lys Thr Pro	624
195 200 205	
ctg caa gtc gcc aaa ggg ggc ctg ggt tta ata ctc aaa aga atc gca Leu Gln Val Ala Lys Gly Gly Leu Gly Leu Ile Leu Lys Arg Ile Ala	672
210 215 220	
gaa agt gaa gag gct tct atg tag Glu Ser Glu Glu Ala Ser Met	696
225 230	

<210> 6
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Gly Lys Leu Asp Glu Leu Lys Glu Ser Ile Leu Ala Asp Lys Ser Leu
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Ala Thr Arg Thr Asp Gln Asp Ser Arg Thr Ala Leu His Trp Ala Cys
35 40 45
Ser Ala Gly His Thr Glu Ile Val Glu Phe Leu Leu Gln Leu Gly Val
50 55 60
Pro Val Asn Glu Lys Asp Asp Ala Gly Trp Ser Pro Leu His Ile Ala
65 70 75 80
Ala Ser Ala Gly Arg Asp Glu Ile Val Lys Ala Leu Leu Ile Lys Gly
85 90 95
Ala Gln Val Asn Ala Val Asn Gln Asn Gly Cys Thr Ala Leu His Tyr
100 105 110
Ala Ala Ser Lys Asn Arg His Glu Ile Ala Val Met Leu Leu Glu Gly
115 120 125
Gly Ala Asn Pro Asp Ala Lys Asn His Tyr Asp Ala Thr Ala Met His
130 135 140
Arg Ala Ala Ala Lys Gly Asn Leu Lys Met Val His Ile Leu Leu Phe
145 150 155 160
Tyr Lys Ala Ser Thr Asn Ile Gln Asp Thr Glu Gly Asn Thr Pro Leu
165 170 175
His Leu Ala Cys Asp Glu Glu Arg Val Glu Glu Ala Lys Leu Leu Val
180 185 190
Thr Gln Gly Ala Ser Ile Tyr Ile Glu Asn Lys Glu Glu Lys Thr Pro
195 200 205
Leu Gln Val Ala Lys Gly Leu Gly Leu Ile Leu Lys Arg Ile Ala
210 215 220
Glu Ser Glu Glu Ala Ser Met
225 230

<210> 7
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<212> PRT
<213> Homo sapiens

<400> 7
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1 5 10 15

<210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 8
cctgtcgctt tacctcccca 20

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 9
tacctcccca cacacagatt 20

<210> 10
<211> 28
<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence: ANK consensus

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<223> P or A

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<222> (6)
<223> L, I or V

<220>
<221> MOD_RES
<222> (8)
<223> A or S

<220>
<221> MOD_RES
<222> (9)
<223> R, Q or K

<220>

<221> MOD_RES
<222> (10)
<223> G or N

<220>
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<223> H or N

<220>
<221> MOD_RES
<222> (12)
<223> V, L or T

<220>
<221> MOD_RES
<222> (13)
<223> E or D

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<223> V, I or M

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<223> V or A

<220>
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<223> K, E or R

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<223> L or V

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<223> D, K, Q or E

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<223> D, N or S

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<223> V, P or I

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<222> (25)
<223> N or D

<220>
<221> MOD_RES
<222> (27)
<223> T, D or N

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1 5 10 15

Xaa Leu Leu Xaa Gly Ala Xaa Xaa Ala Xaa Lys
20 25

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<211> 33
<212> PRT
<213> Homo sapiens

<220>
<223> ankyrin repeat

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1 5 10 15

Ile Val Glu Phe Leu Leu Gln Leu Gly Val Pro Val Asn Asp Lys Asp
20 25 30

Asp

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<211> 33
<212> PRT
<213> Homo sapiens

<220>
<223> ankyrin repeat

<400> 12
Ala Gly Trp Ser Pro Leu His Ile Ala Ala Ser Ala Gly Arg Asp Glu
1 5 10 15

Ile Val Lys Ala Leu Leu Gly Lys Gly Ala Gln Val Asn Ala Val Asn
20 25 30

Gln

<210> 13
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<223> ankyrin repeat

<400> 13

Asn	Gly	Cys	Thr	Pro	Leu	His	Tyr	Ala	Ala	Ser	Lys	Asn	Arg	His	Glu
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Ile	Ala	Val	Met	Leu	Leu	Glu	Gly	Gly	Ala	Asn	Pro	Asp	Ala	Lys	Asp
				20				25					30		

His

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<212> PRT

<213> Homo sapiens

<220>

<223> ankyrin repeat

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Tyr	Glu	Ala	Thr	Ala	Met	His	Arg	Ala	Ala	Lys	Gly	Asn	Leu	Lys
1				5				10				15		

Met	Ile	His	Ile	Leu	Leu	Tyr	Tyr	Lys	Ala	Ser	Thr	Asn	Ile	Gln	Asp
				20				25				30			

Thr

<210> 15

<211> 33

<212> PRT

<213> Homo sapiens

<220>

<223> ankyrin repeat

<400> 15

Glu	Gly	Asn	Thr	Pro	Leu	His	Leu	Ala	Cys	Asp	Glu	Glu	Arg	Val	Glu
1				5				10				15			

Glu	Ala	Lys	Leu	Leu	Val	Ser	Gln	Gly	Ala	Ser	Ile	Tyr	Ile	Glu	Asn
			20				25				30				

Lys

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<212> PRT

<213> Homo sapiens

<220>

<223> ankyrin repeat

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Glu	Glu	Lys	Thr	Pro	Leu	Gln	Val	Ala	Lys	Gly	Gly	Leu	Gly	Leu	Ile
1				5				10				15			

Leu	Lys	Arg	Met	Val	Glu	Gly
			20			